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Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,

Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,

Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,

Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,

Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,

Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,

Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,

Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Saaski,D.,

Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Tskahashi,F.,

Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,

Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,

Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and

Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
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DNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.2. Second Strand cDNA was prepared with the primer
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Shibata, K.,
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="16 days embryo"
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/clone="8430417G17"
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/db_xref="MGD:MGT:1909149"
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77.7%;
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Pred. No. 9.4e-193;
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RESULT 2
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  652 bp mi
BB613812 RIKEN full-length enriched,
musculus cDNA clone 4831431E11 5', mF
BB613812
                                                                               Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
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EST.
                                         Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse
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Sciurognathi; Muridae;
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Best Local Similarity
                                                                                                                                                                                                                                                                                 Matches 533;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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10 (11), 1
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Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e mouse tissues.
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GCCTGCTTTCCCAGTTTGGACTTATGCCTCTGACAGCTTATCTGTTAGCCATTGGCTTCG
                                          GACTGCTCTGCCAGTTTGGGCTCATGCCTTTTACAGCTTATCTCCTGGCCATTAGCTTTT
                                                                                                                                        GTTCCGTGGAGATCCGGAAGCTGTGGTCGCACATCAGGAGACCCTGGGGCATTGCTGTGG
                                                                                                                                                                                        AGCTGCTTTTTACAGTGCTCTCGGCTGTGATGGTGGGTTTTGGTCATGTTCTCTTTTTGGAT
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                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 primed with a primer [5' GAGAGAGAGAGAGAGAGATOVA 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Site 1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contributed to prepare mouse tissues. 1st strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dev_stage="0 day neonate"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="head"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="mixed"
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lone="4831431E11"
                                                                                                                                                                                                                                                                                                        39.7%;
81.7%;
                                                                                                                                                                                                                                                                               Score 450.4; DB 10
Pred. No. 2.8e-119;
D; Mismatches 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BG872314
BG872314.1 GI:
EST.
                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
plate: LLAM10841 row: j column: 20
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602790977F1 NCI_CGAP_
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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     222
                                                                                                                                                                                                                                           quality sequence stop:
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/db_xref="taxon:10090"
/clone="IMAGE:492227"
/clone="b="NCI_CGAP_SG2"
/clone_lib="NCI_CGAP_SG2"
/lab_host="DH10B (T1_phage-resistant)"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_NotI; Site_2: Sali; Cloned unidirectionally. Primer: Oli dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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Best Local Similarity 73.8
----- 458; Conservative
   JOURNAL
MEDLINE
                                                           TITLE
                                                                                                                                                                      AUTHORS
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                                                                                         1 (bases 1 to 356)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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CM2-HT0630-220300-125-f05 HT0630 Homo
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                                                         Shotgun sequencing of the human transcriptome with ORF
                                                                            Simpson, A.J.
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mRNA sequence. EST 22-JUN-2000

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                                                                                                                                BB625035 RIKEN full-length enriched, adult male cDNA clone 9030619K19 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brazil
Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 and
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 658)
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                                                        Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0630"
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It,
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuu
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., e Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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Tel: 81-45-503-9222
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e mouse tissues.
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Computer-based methods for the mouse full-length cDNA
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Lrom Lambda
BamHI"
                                 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                                                                                                                                  /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                          dev_stage="adult"
lab_host="DH10B"
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'db_xref="taxon:10090"
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Y., Kira, A. and
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Ohazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Sinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y., RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
                 Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group,
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (R
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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BB664585
                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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genome-res@gsc.riken.go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                662 bp mRNA linear EST RIKEN full-length enriched, 0 day neonate lung cDNA clone E030047A18 5', mRNA sequence.
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Pred. No. 1.1e-46;
0; Mismatches 195;
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Best Local Similarity
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199
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Carninci,P., Shibata,Y., Hayaftau,N., Sugahara,Y., Shibata,K., Itoh
Carninci,P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-630 (2000)
wagji,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Ns., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizaw,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sug,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Genome Sequences. Mamm.
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                                     CACATCAGGAGACCCTGGGGCATTGCTGTGGGACTGCTCTGCCAGTTTGGGCTCATGCCT
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                                                                                    ATGGTGGGGGGGTAATGCTCACTTTTGGATGTAGAGCGGACAGTGAGAATCTCTGGTTG
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a 137 c
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/lab_host="DH10B"
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/clone="E030047A18"
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                                                                                                                                                                                                                                                                                                                                                              17.6%;
70.7%;
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Pred. No. 1.1e-46;
0; Mismatches 110;
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REFERENCE
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                                                                                                                                                                                                                                277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Kiyoshi Naruse
Department of Biological Sciences
Graduate School of Science, Unive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU176916 Sugano-Kawakami 5' end enriched cDNA library (OLA) from HNI Oryzias latipes cDNA clone OLA22.10c similar to pir|A49876| Na+-dependent bile acid transporter, ileal - golden hamster, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: naruse@biol.s.u-tokyo.ac.jp
This clone was isolated from Sugano-Kawakami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 81-3-5841-4443
Fax: 81-3-5841-4410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hongo 7-3-1, Bunkyo-ku,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Naruse, K., Mitani, H. and Tanaka, M. Medaka EST Project in University of Tokyo (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryzias latipes
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                                                                                                                                                                                                                                               Similarity
 GCTATTGCTGTTCTCATCATGGGCTGCTGCCCGGGGGGCACCATCTCTAACATTTTCACC 348
                                                               GGGCTCATGCCTTTTACAGCTTATCTCCTGGCCATTAGCTTTTCTCTGAAGCCAGTCCAA 288
                                                                                                                 AAGCTGTGGTCGCACATCAGGAGACCCTGGGGCATTGCTGTGGGACTGCTCTGCCAGTTT
                                                                                                                                                               GTGCTCACTGTCATGCTCGCCATGGTCATGTTCGCCATGGGCTGCACGGTGGACTTCTGG
                                                                                                                                                                                     GTGTCCACTGTGATGAGGGGCTGCTCATGTTCTCTTTGGGATGTTCCGTGGAGATCCGG
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                                GGCATCATGCCCTTCACGGCCTTCGCCCTGTCCCTCGCCTTCAACGTTCTGCCTGTGCAG
                                                                                               AAGCTGTGGGGTCACATCAGGAGACCTTGGGGGCATCGTCATCGGCTTCATCTGCCAGTTT
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                                                                                                                                                                                                                                                                                                                106
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                             /tissue_type="whole body"
/dev_stage="adult"
200 c 167 g 169
                                                                                                                                                                                                                                                                                                                                                               /clone="OLa22.10c"
                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:8090"
                                                                                                                                                                                                                                                                                                                                                                                                                                strain="HNI"
                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Oryzias latipes"
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                                                                                                                                                                                                                                            Score 194.2;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nce, University
Tokyo 113-0033,
                                                                                                                                                                                                                              Mismatches 138;
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Best Local :
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                                                                                                                                      325;
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11518 row: k column: 06
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603057222F1 NIH_MGC_122 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
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                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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                                                            ATAACATCCTAAGTGTGGTCCTAAGTACGGTGCTGACCATCCTGTTGGCCCTTGGTGATGT
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                                                                                            ATGGAAACCTGGAGCTCGTTTTCACAGTGGTGTCCACTGTGATGATGGGGGCTGCTCATGT 139
                                                                                                                                                                                                                                  181
                                                                                                                                    Conservative
                                                                                                                                                                                                                          /note-"Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone_lib="NIH_MGC_122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'db_xref="taxon:9606"
'clone="IMAGE:5206781"
                                                                                                                                                                                                                                                                                                                                                                                                                                              lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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                                                                                                                                  0,
                                                                                                                                  Score 189; DB 13;
Pred. No. 1.7e-43;
D; Mismatches 190;
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sapiens
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                                                                                                                                   This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM2-HT0285-081 199-028-a09&t3=1999-11-08&t4=1) Seq primer: puc 18 forward High Primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 274)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rud Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE151388 2
CM2-HT0285-081199-028-a09
BE151388 GI:8614109
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                                                                                                                                                                                                                                               Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simpson, A.J.
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                                                                                                 quality sequence stop: 109
                                                                                                                        quality sequence start: 16
/clone_lib="HT0285"
                     organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                     Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                              Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For
Clones availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased i
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering)
Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1998)
Other_GSSs: RPCI11-2407.TKBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Golden, K., Berry, K., Granger, Venter, J.C.
Use of BAC End Sequences for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buteria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 543)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.
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RPCI11-2407.TKBF RPCI-11 Homo
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/clone_lib="RPCI-11"
/sex="Male"
                                     /db_xref="GDB:7509174"
/db_xref="taxon:9606"
/clone="RPCI-11-2407"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Adult"
                                                                                                 organism="Homo sapiens"
                                                                                                                                           ocation/Qualifiers
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Pred. No. 3.5e-42;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188;
                                                                                                                                                                                                                                                                                                                                                                         USDA, ARS, US Meat
PO Box 166, Clay Co
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 538)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T. Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., and Keele,J.W.
                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                                                                          FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa
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x 166, Clay Center, NE 68933-0166, USA
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                                                                                                          /organism="Sus scrofa"
/db xref="taxon:9823"
/clone_lib="MARC IPIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                      /note="Vector: pCMV SPORT6; Site
Library made from pooled tissue
and 30 embryos."
142 c 153 g 136 t
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RPCI11 Human Male BAC Library"
118 c 97 g 160 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Lymphocytes"
/note="Vector: pBACe3.6;
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 14.5%;
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Pred. No. 1.1
 Score 164.6;
                                                                            pCMV SPORT6; Site_1: NotI; Site_2: rom pooled tissue from day 11, 13,
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Sus.
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IMAGE:2192673 5' similar to TR:P70172 F
BILE ACID TRANSPORTER ;, mRNA sequence.
AM107022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 686)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Thessing, B., Allen, M., Bowers, Y., Pe, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ri, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                             Seq primer: custom primer used High quality sequence stop: 49:
                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW107022.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGGAGACCCTGGGGCATTGCTGTGGGACTGCTCTTGCCCAGTTTTGGGCTCATGCCTTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTCTGCATTTATCTCTACACC 447
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/note="Organ: kidney; Vector:
(CACTGTGTG); Site_2: DraIII (
was primed with an oligo(dT) |
                                                                                                                                                                                                           1. .686
                                                                                                                                                                                                                           ity sequence stop: .
Location/Qualifiers
                                                       dev_stage="adult"
lab_host="DH10B"
                                                                                                             /db_xref="taxon:10090"
/clone="IMAGE:2192673"
/clone_lib="Sugano mouse
                                                                                             sex="female"
                                                                                                                                                                                         organism="Mus musculus"
                                                                                                                                                                         strain="C57BL"
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72 P70172 ILEAL NA+-DEPE
                 : pME18S-FL3; Site_1: DraIII
(CACCATGTG); 1st strand cDNA
                                                                                                                                                                                                                                                                                                                                                                                                      Louis, MO 63108,
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Schurk,R., Ritter
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JOURNAL COMMENT
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                   1 (bases 1 to 666)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)
                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                      BB625042 RIKEN full-length enriched, adult cDNA clone 9030621119 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                 BB625042
BB625042.1 GI:15398453
                                                                                                                                                                                                                                                                                                                                     house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGCAATTCTCAATACAGTGATGAGCACTGTGCTCACCATCCTCTTAGCCATGGTGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTCTCTGGTTGTCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTACACCTGGTCCTGGAGTCTTCAGCAGAATCTCACCATTCCTTATCAGAACATAGGAA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTAGCATGACCACTTGCTCCACACTGCTTGCCCTTTGGAATGATGCCTCTNTGCCTCTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGAGGAACTGGCTCCAATATCCTGGCCTATTGGATAGATGGCGACATGGACCTCAGTG
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  Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [ATCTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a Draili adaptor [TTTTGGCCTACTGG], digested and cloned into distinct braili sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG) Xhol should
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 162.4; DB 1
Pred. No. 8.7e-36;
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ATGGAAACCTGGAGCTCGTTTTCACAGTGGTGTCCACTGTGATGATGGGGGCTGCTCATGT 139 ATGCAATTCTCAATACAGTGATGAGCACTGTGCTCACCATCCTCTAGCCATGGTGATGT

Matches

240; 80

Query Match Best Local Similarity

13.2%; 61.4%;

Pred. No. 5.1); Mismatches Score 149.4; DB 1 Pred. No. 5.1e-32;

DB 10;

Length

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Gaps

244

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185

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Yamanaka, I. Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizaw, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T. Ishii, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genome Exploration Research Group,
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                               147
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                                                       from Lambda
BamHI"
                                                                                                                                                                    Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                      Vector:
                                                                                                                                                                                                                                                                                                                                                         contributed to prepare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="colon"
/dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="9030621I19"
                                                                             J. cDNA was cloned into the XhoI and BamHI sites. ctor: a modified pBluescript KS(+) after bulk excision om Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                                  146 c
                               165
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REFERENCE
AUTHORS
TITLE
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BI149148
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence
BI149148
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602912378F1_NCI_CGAP_Li9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Plate: LLAM11145 row: k column:
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1 (bases 1 to 919)
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 quality sequence start: 9
                                     Conservative
                                                                                                                  /db_xref="taxon:10000"
/dlone="IMAGE:553578"
/clone="Ib="NCI CGAP_Li9"
/clone_lib="NCI CGAP_Li9"
/lab host="DH10B (TI phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 sb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 265 c 230 g 222 t
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                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
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ACCESSION
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                                                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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602028555F1 NCI_CGAP_Li9
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 876)
                                                                                                                                                                                                         quality sequence stop: 684.
/strain="FVB/N"
/db xref="taxon:1090"
/db xref="taxon:1090"
/clone="IMAGE:4163893"
/clone_lib="NCI_CGAP_Li9"
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B_(TI_phage-resistant)"
/lab_host="DH10B_(TI_phage-resistant)"
/note="Organ: liver; Vector: pcMV-SPDRT6; Site_1: NotI;
/note="Organ: liver; Vector: pcMV-SPDRT6; Site_1: NotI;
/note="Cstali; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                      location/Qualifiers
                                                                                                                                              organism="Mus musculus"
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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Best Local Similarity
Matches 288; Conserv
                                     595 Grigingerecercciccincreerecicecaer 629
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                                                                                                                                                                    543 AAGGTGCCCTACAAAGGCATTATGTTATCACTCGTCATGGTTCTCATTCCTTGCGCCATA 602
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                                                                                                                                                                                                                                                    423 AAGGGGGACATGAACCTCAGCATNGTGATGACCACCTGCTCCAGCTTCACTGCCTTGGGC
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663 ATCATCACTTTCTCCCTCTCTGTGGCTGTCACAGT 697
                                                                                                                                                                                                                                                                                                                                                                                                                           363 ATCCTCATCTGCGGCTGCTCTCCTGGGGGGAACCTGTCTAACCTCTTCACCCTGGCCATG
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                                                                                                                 GGTGTCTATGTGAATTACAGATGGCCAAAAACAATCCAAAATCATTCTCAAGATTGGGGCC
                                                                                    ACCATTCCTTATCAGAACATAGGAATTACCCTTGTGTGCCTGACCATTCCTGTGGCCTTT
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Search completed: June 9, 2003, 07:06:01 Job time: 1872 secs